RAW SEQUENCE LISTING   DATE: 10/10/2003
PATENT APPLICATION: **US/09/502,498B**   TIME: 10:59:17

Input Set : **A:\sequence listing 407C2.txt**
Output Set: **N:\CRF4\10102003\I502498B.raw**

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 3 <110> APPLICANT: Kilian, Andrzej
 4         Bowtell, David
 6 <120> TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
 7         THEREOF
 9 <130> FILE REFERENCE: 407C2
11 <140> CURRENT APPLICATION NUMBER: 09/502,498B
12 <141> CURRENT FILING DATE: 2000-02-11
14 <160> NUMBER OF SEQ ID NOS: 155
16 <170> SOFTWARE: PatentIn Ver. 2.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 3964
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <400> SEQUENCE: 1
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25 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
26 cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
27 gacgcacggc cgccccccgc cgcccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
28 gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
29 ttcgcgctgc tggacggggc ccgcgggggc cccccccgagg ccttcaccac cagcgtgcgc 360
30 agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgtg ggggctgctg 420
31 ttgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
32 ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
33 gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
34 cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
35 gcgaggaggc gcggggggcag tgccagccga agtctgccgt gcccaagag gcccaggcgt 720
36 ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
37 aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
38 gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
39 cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
40 tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
41 ctgcggcccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
42 gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
43 cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
44 gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
45 ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
46 gaggacacag accccccgtcg cctggtgcag ctgctccgcc agcacagcag ccccctggcag 1380
47 gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
48 aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
49 gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcggggctg cgcttggctg 1560
50 cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
51 ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
52 ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
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53 tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
54 ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
55 ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
56 ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
57 ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
58 ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100
59 gacccgccgc ctgagctgta ctttgtcaag gtggatgtga cgggcgcgta cgacaccatc 2160
60 ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aaccccagaa cacgtactgc 2220
61 gtgcgtcggt atgccgtggt ccagaaggcc gcccatgggc acgtccgcaa ggccttcaag 2280
62 agccacgtct ctaccttgac agacctccag ccgtacatgc gacagttcgt ggctcacctg 2340
63 caggagacca gcccgctgag ggatgccgtc gtcatcgagc agagctcctc cctgaatgag 2400
64 gccagcagtg gcctcttcga cgtcttccta cgcttcatgt gccaccacgc cgtgcgcatc 2460
65 aggggcaagt cctacgtcca gtgccagggg atcccgcagg gctccatcct ctccacgctg 2520
66 ctctgcagcc tgtgctacgg cgacatggag aacaagctgt ttgcgggggat tcggcgggac 2580
67 gggctgctcc tgcgtttggt ggatgatttc ttgttggtga cacctcacct cacccacgcg 2640
68 aaaaccttcc tcaggaccct ggtccgaggt gtccctgagt atggctgcgt ggtgaacttg 2700
69 cggaagacag tggtgaactt ccctgtagaa gacgaggccc tgggtggcac ggctttttgtt 2760
70 cagatgccgg cccacggcct attcccctgg tgcggcctgc tgctggatac ccggaccctg 2820
71 gaggtgcaga gcgactactc cagctatgcc cggacctcca tcagagccag tctcaccttc 2880
72 aaccgcggct tcaaggctgg gaggaacatg cgtcgcaaac tctttggggt cttgcggctg 2940
73 aagtgtcaca gcctgtttct ggatttgcag gtgaacagcc tccagacggt gtgcaccaac 3000
74 atctacaaga tcctcctgct gcaggcgtac aggtttcacg catgtgtgct gcagctccca 3060
75 tttcatcagc aagtttggaa gaaccccaca ttttttcctgc gcgtcatctc tgacacggcc 3120
76 tccctctgct actccatcct gaaagccaag aacgcaggga tgtcgctggg ggccaagggc 3180
77 gccgccggcc ctctgccctc cgaggccgtg cagtggctgt gccaccaagc attcctgctc 3240
78 aagctgactc gacaccgtgt cacctacgtg ccactcctgg ggtcactcag gacagcccag 3300
79 acgcagctga gtcggaagct cccggggacg acgctgactg ccctggaggc cgcagccaac 3360
80 ccggcactgc cctcagactt caagaccatc ctggactgat ggccacccgc ccacagccag 3420
81 gccgagagca gacaccagca gccctgtcac gccgggctct acgtcccagg gagggagggg 3480
82 cggcccacac ccaggcccgc accgctggga gtctgaggcc tgagtgagtg tttggccgag 3540
83 gcctgcatgt ccggctgaag gctgagtgtc cggctgaggc ctgagcgagt gtccagccaa 3600
84 gggctgagtg tccagcacac ctgccgtctt cacttcccca caggctggcg ctcggctcca 3660
85 ccccagggcc agcttttcct caccaggagc ccggcttcca ctccccacat aggaatagtc 3720
86 catccccaga ttcgccattg ttcacccctc gccctgccct cctttgcctt ccaccccac 3780
87 catccaggtg gagaccctga gaaggaccct gggagctctg ggaatttgga gtgaccaaag 3840
88 gtgtgccctg tacacaggcg aggaccctgc acctggatgg gggtccctgt gggtcaaatt 3900
89 ggggggaggt gctgtgggag taaaatactg aatatatgag tttttcagtt ttgaaaaaaa 3960
90 aaaa                                                            3964
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 1132
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 2
98 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
99  1               5                  10                  15
101 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
102              20                  25                  30
104 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
105              35                  40                  45
```

```
107 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
108         50              55              60
110 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
111  65              70              75                      80
113 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
114             85              90                      95
116 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
117         100             105             110
119 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
120         115             120             125
122 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
123     130             135             140
125 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
126 145             150             155             160
128 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
129             165             170             175
131 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
132         180             185             190
134 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
135         195             200             205
137 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
138     210             215             220
140 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
141 225             230             235             240
143 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
144             245             250             255
146 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
147         260             265             270
149 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
150         275             280             285
152 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
153     290             295             300
155 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
156 305             310             315             320
158 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
159             325             330             335
161 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
162         340             345             350
164 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
165         355             360             365
167 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
168     370             375             380
170 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
171 385             390             395             400
173 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
174             405             410             415
176 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
177             420             425             430
179 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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Input Set : **A:\sequence listing 407C2.txt**
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180         435                  440                  445
182 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
183         450                  455                  460
185 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
186 465                  470                  475                  480
188 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
189                  485                  490                  495
191 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
192                  500                  505                  510
194 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
195                  515                  520                  525
197 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
198         530                  535                  540
200 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
201 545                  550                  555                  560
203 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
204                  565                  570                  575
206 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
207                  580                  585                  590
209 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
210         595                  600                  605
212 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
213         610                  615                  620
215 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
216 625                  630                  635                  640
218 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
219                  645                  650                  655
221 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
222         660                  665                  670
224 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
225         675                  680                  685
227 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
228         690                  695                  700
230 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
231 705                  710                  715                  720
233 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
234         725                  730                  735
236 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
237         740                  745                  750
239 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
240         755                  760                  765
242 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
243         770                  775                  780
245 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
246 785                  790                  795                  800
248 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
249                  805                  810                  815
251 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
252         820                  825                  830
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Input Set : **A:\sequence listing 407C2.txt**
Output Set: **N:\CRF4\10102003\I502498B.raw**

```
254 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
255         835               840             845
257 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
258     850               855             860
260 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
261 865               870             875             880
263 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
264               885               890             895
266 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
267         900               905             910
269 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
270         915               920             925
272 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
273     930               935             940
275 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
276 945               950             955             960
278 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
279               965               970             975
281 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
282         980               985             990
284 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
285         995               1000             1005
287 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
288     1010               1015             1020
290 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
291 1025               1030             1035             1040
293 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
294               1045               1050             1055
296 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
297         1060               1065             1070
299 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
300         1075               1080             1085
302 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
303     1090               1095             1100
305 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
306 1105               1110             1115             1120
308 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
309               1125               1130
312 <210> SEQ ID NO: 3
313 <211> LENGTH: 1031
314 <212> TYPE: PRT
315 <213> ORGANISM: Euplotes aediculatus
317 <400> SEQUENCE: 3
318 Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
319  1             5               10               15
321 Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
322             20               25               30
324 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
325         35               40               45
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/10/2003
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 1,2,3,4,5,6,7
Seq#:34; N Pos. 1767,1768,1769
Seq#:51; N Pos. 1871,1872,1873
Seq#:91; Xaa Pos. 2,3,4,5
Seq#:93; Xaa Pos. 2,3,4,5,7,8
Seq#:95; N Pos. 1,2,3,5,9,10,11,12,13,14

VERIFICATION SUMMARY   DATE: 10/10/2003
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Input Set : **A:\sequence listing 407C2.txt**
Output Set: **N:\CRF4\10102003\I502498B.raw**

```
L:1039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:1356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:1740
L:3364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:1860
L:9327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:0
L:9364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:93 after pos.:0
L:9406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95 after pos.:0
```